

Amendments to the Specification:

Please amend the paragraph on page 7, beginning at line 15 as follows:

The sequences and related information of the genes described herein are available in the public databases. Tables 1-6 provide the Accession numbers and name for each of the sequences. Each Accession Number corresponds to a sequence in the attached sequence listing. The sequences and related information of the genes listed in the Tables according to their GenBank identifiers are expressly incorporated herein as of the filing date of this application, as are sequences in the databases related to those herein described, such as fragments, variant sequences, etc. [(see: www.ncbi.nlm.gov).]

Please amend the paragraph on page 30, beginning at line 14 as follows:

The expression profiles [of] of one or more of the individual genes of Tables 1-6 are used as molecular or diagnostic markers to evaluate the disease status of a patient sample. In one embodiment, a patient prostate tissue sample is processed as described herein to produce total cellular or mRNA. The RNA is hybridized to a chip [continuing] comprising probes that specifically hybridize to one or more, or two or more of the genes in Tables 1-6. The overall expression profile generated, or the expression levels of individual genes are then compared to the profiles as described in Tables 1-6 to determine the disease or hyperplastic state of the patient sample.